

SEQUENCE LISTING

<110> The Horticulture and Food Research Institute of NZ

<120> Seedless Fruit Production

<130> 26329 MRB

<140>

<141>

<150> NZ337688

<151> 1999-09-07

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 868

<212> DNA

<213> Malus domestica

<220>

<221> CDS

<222> (1)..(648)

<400> 1

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Met Gly Arg Gly Lys Val Glu Ile Lys Arg Ile Glu Asn Ser Ser Asn	
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agg cag gtg acc tac tcc aag agg agg aat ggg att atc aag aag gca	96
Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Ile Lys Lys Ala	
20 25 30	
aag gag atc act gtt cta tgt gat gct aaa gta tct ctt atc att tat	144
Lys Glu Ile Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Ile Tyr	
35 40 45	
tct agc tct ggg aag atg gtt gaa tac tgc agc cct tca act acg ctg	192
Ser Ser Ser Gly Lys Met Val Glu Tyr Cys Ser Pro Ser Thr Thr Leu	
50 55 60	
aca gaa atc ttg gac aaa tac cat gga caa tct ggg aag aag ttg tgg	240
Thr Glu Ile Leu Asp Lys Tyr His Gly Gln Ser Gly Lys Lys Leu Trp	
65 70 75 80	
gat gct aag cat gag aac ctc agc aat gaa gtg gat aga gtc aag aaa	288
Asp Ala Lys His Glu Asn Leu Ser Asn Glu Val Asp Arg Val Lys Lys	
85 90 95	
gac aat gac agc atg caa gta gag ctc agg cat ctg aag gga gag gat	336
Asp Asn Asp Ser Met Gln Val Glu Leu Arg His Leu Lys Gly Glu Asp	
100 105 110	
atc aca tca ttg aac cat gta gag ctg atg gcc tta gag gaa gca ctt	384

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Ile Thr Ser Leu Asn His Val Glu Leu Met Ala Leu Glu Glu Ala Leu
      115                      120                      125

gaa aat ggc ctt aca agt atc cgg gac aag cag tcc aag ttc gtc gac   432
Glu Asn Gly Leu Thr Ser Ile Arg Asp Lys Gln Ser Lys Phe Val Asp
      130                      135                      140

atg atg aga gac aat gga aag gca ctg gaa gat gag aat aag cgc ctc   480
Met Met Arg Asp Asn Gly Lys Ala Leu Glu Asp Glu Asn Lys Arg Leu
      145                      150                      155                      160

act tat gag ctg caa aaa caa cag gag atg aaa ata aaa gag aat gtg   528
Thr Tyr Glu Leu Gln Lys Gln Gln Glu Met Lys Ile Lys Glu Asn Val
      165                      170                      175

aga aac atg gaa aat ggg tat cat cag agg cag ctg ggg aac tac aac   576
Arg Asn Met Glu Asn Gly Tyr His Gln Arg Gln Leu Gly Asn Tyr Asn
      180                      185                      190

aac aac cag cag cag ata cct ttt gcc ttc cgc gtg cag cct att cag   624
Asn Asn Gln Gln Gln Ile Pro Phe Ala Phe Arg Val Gln Pro Ile Gln
      195                      200                      205

cca aat ctc cag gag aga atc taa ttagatatat cttgcatttg catgctcttt   678
Pro Asn Leu Gln Glu Arg Ile
      210                      215

ctaactagtt atattatctc tccacctctc tctctctttt catctgtcaa ggagttctta 738

agtttatgtc agatttccaa tggtttgtaa tggaattagc ttcgttatga ggctttgttg 798

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<210> 2
<211> 215
<212> PRT
<213> Malus domestica

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<400> 2
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Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Ile Lys Lys Ala
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Lys Glu Ile Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Ile Tyr
      35      40      45
Ser Ser Ser Gly Lys Met Val Glu Tyr Cys Ser Pro Ser Thr Thr Leu
      50      55      60
Thr Glu Ile Leu Asp Lys Tyr His Gly Gln Ser Gly Lys Lys Leu Trp
      65      70      75      80
Asp Ala Lys His Glu Asn Leu Ser Asn Glu Val Asp Arg Val Lys Lys
      85      90      95
Asp Asn Asp Ser Met Gln Val Glu Leu Arg His Leu Lys Gly Glu Asp
      100      105      110
Ile Thr Ser Leu Asn His Val Glu Leu Met Ala Leu Glu Glu Ala Leu

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		115					120					125			
Glu	Asn	Gly	Leu	Thr	Ser	Ile	Arg	Asp	Lys	Gln	Ser	Lys	Phe	Val	Asp
		130					135					140			
Met	Met	Arg	Asp	Asn	Gly	Lys	Ala	Leu	Glu	Asp	Glu	Asn	Lys	Arg	Leu
145					150					155					160
Thr	Tyr	Glu	Leu	Gln	Lys	Gln	Gln	Glu	Met	Lys	Ile	Lys	Glu	Asn	Val
				165					170					175	
Arg	Asn	Met	Glu	Asn	Gly	Tyr	His	Gln	Arg	Gln	Leu	Gly	Asn	Tyr	Asn
			180					185					190		
Asn	Asn	Gln	Gln	Gln	Ile	Pro	Phe	Ala	Phe	Arg	Val	Gln	Pro	Ile	Gln
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Pro	Asn	Leu	Gln	Glu	Arg	Ile									
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<210> 3
<211> 982
<212> DNA
<213> Malus domestica
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<220>  
<221> CDS  
<222> (1) .. (699)
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Met	Ala	Arg	Gly	Lys	Ile	Glu	Ile	Lys	Leu	Ile	Glu	Asn	Gln	Thr	Asn		
1				5					10					15			
agg	cag	gtg	acc	tac	tcc	aag	aga	aga	aat	ggg	atc	ttc	aag	aag	gct		96
Arg	Gln	Val	Thr	Tyr	Ser	Lys	Arg	Arg	Asn	Gly	Ile	Phe	Lys	Lys	Ala		
			20					25					30				
cag	gag	ctc	acc	gtt	ctc	tgt	gat	gcc	aag	gtc	tcc	ctc	att	atg	ctc		144
Gln	Glu	Leu	Thr	Val	Leu	Cys	Asp	Ala	Lys	Val	Ser	Leu	Ile	Met	Leu		
			35				40					45					
tcc	aac	act	aat	aaa	atg	cac	gag	tat	atc	agc	cct	acc	act	acg	acc		192
Ser	Asn	Thr	Asn	Lys	Met	His	Glu	Tyr	Ile	Ser	Pro	Thr	Thr	Thr	Thr		
	50					55					60						
aag	agt	atg	tat	gat	gac	tat	cag	aaa	act	atg	ggg	atc	gat	ctg	tgg		240
Lys	Ser	Met	Tyr	Asp	Asp	Tyr	Gln	Lys	Thr	Met	Gly	Ile	Asp	Leu	Trp		
65				70					75					80			
agg	aca	cac	gag	gag	tcg	atg	aaa	gac	acc	ttg	tgg	aag	ttg	aaa	gag		288
Arg	Thr	His	Glu	Glu	Ser	Met	Lys	Asp	Thr	Leu	Trp	Lys	Leu	Lys	Glu		
				85				90						95			
atc	aac	aat	aag	ctg	agg	aga	gag	atc	agg	cag	agg	ttg	ggc	cat	gat		336
Ile	Asn	Asn	Lys	Leu	Arg	Arg	Glu	Ile	Arg	Gln	Arg	Leu	Gly	His	Asp		
			100				105						110				
cta	aat	ggc	ctg	agc	ttt	gac	gag	ctg	gct	tct	ctt	gac	gat	gag	atg		384
Leu	Asn	Gly	Leu	Ser	Phe	Asp	Glu	Leu	Ala	Ser	Leu	Asp	Asp	Glu	Met		
		115					120					125					

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cag tct tcc ttg gat gcc ata cgt caa agg aag tac cat gtg atc aaa 432
Gln Ser Ser Leu Asp Ala Ile Arg Gln Arg Lys Tyr His Val Ile Lys
130 135 140

act cag acg gag acc acc aag aag aag gtt aag aac ttg gag caa aga 480
Thr Gln Thr Glu Thr Thr Lys Lys Lys Val Lys Asn Leu Glu Gln Arg
145 150 155 160

aga gga aac atg ctg cat ggc tat ttt gac cag gaa gca gcc ggc gag 528
Arg Gly Asn Met Leu His Gly Tyr Phe Asp Gln Glu Ala Ala Gly Glu
165 170 175

gat cca cag tat ggt tat gag gac aat gag gga gac tac gaa tct gca 576
Asp Pro Gln Tyr Gly Tyr Glu Asp Asn Glu Gly Asp Tyr Glu Ser Ala
180 185 190

ctt gca ttg tca aat ggg gcg aat aac ttg tac act ttc cac ctc cac 624
Leu Ala Leu Ser Asn Gly Ala Asn Asn Leu Tyr Thr Phe His Leu His
195 200 205

cac cct aac ctc cac cac gga gga agc tcg ctc ggc tcc tcc att act 672
His Pro Asn Leu His His Gly Gly Ser Ser Leu Gly Ser Ser Ile Thr
210 215 220

cat ctg cac gat ctc cgc ctt gct tga tcgtgatctg agatatgatt 719
His Leu His Asp Leu Arg Leu Ala
225 230

aatcatcact aagttatata ttaaggtcac ttataactgc ttttgctcta aagtgtttgc 779

ttggtgacta tctttaggca aggagttaga cttggactac ctctgaaaac agatgcataa 839

atatgtgtgt ggtgttttaa tcaatgatag cactaaaaaa atccgcgccc ttgttgcttg 899

tggggtttggt tgtataatta atacttctat tctatatata tcatggcaga cattgctttt 959

gataaaaaaa aaaaaaaaaa aaa 982

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<210> 4
<211> 232
<212> PRT
<213> Malus domestica

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<400> 4
Met Ala Arg Gly Lys Ile Glu Ile Lys Leu Ile Glu Asn Gln Thr Asn
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Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala
20 25 30
Gln Glu Leu Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Met Leu
35 40 45
Ser Asn Thr Asn Lys Met His Glu Tyr Ile Ser Pro Thr Thr Thr Thr
50 55 60
Lys Ser Met Tyr Asp Asp Tyr Gln Lys Thr Met Gly Ile Asp Leu Trp
65 70 75 80
Arg Thr His Glu Glu Ser Met Lys Asp Thr Leu Trp Lys Leu Lys Glu

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[illegible]

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<210> 5
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<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Made in lab

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<221> allele
<222> (14)
<223> n represents a, c, g, or t.
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<220>
<221> allele
<222> (17)
<223> n represents a, c, g, or t.
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<220>
<221> allele
<222> (20)
<223> n represents a, c, g, or t.
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cggaattcat gggnmgnnggn aarrt
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25

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<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Made in lab

<220>

<221> allele  
<222> (19)  
<223> n represents a, c, g, or t.

<220>  
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<220>  
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<222> (28)  
<223> n represents a, c, g, or t.

<400> 6  
cgctcgagga tccggytgna tnggytgnac 30

<210> 7  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Made in lab

<400> 7  
gagagagaac tagtctcgag 20